



SEQUENCE LISTING

<110> CROCE, Carlo M.
ISHII, Hideshi

<120> COMPOSITIONS, KITS, AND METHODS RELATING TO THE HUMAN
FEZ1 GENE, A NOVEL TUMOR SUPPRESSOR GENE

<130> 9855-30U1 (209855.0081)

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<150> US 60/121,537

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<213> Homo sapiens

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<211> 596

<212> PRT

<213> Homo sapiens

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Lys Leu Asn Arg Tyr Ser Asp Gly Leu Leu Arg Phe Gly Phe Ser Gln
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Asp Ser Gly His Gly Lys Ser Ser Ser Lys Met Gly Lys Ser Glu Asp
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Phe Phe Tyr Ile Lys Val Ser Gln Lys Ala Arg Gly Ser His His Pro
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Asp Phe Asp Pro Ser Thr Pro Pro Lys Leu Met Pro Phe Ser Asn Gln

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<213> Homo sapiens

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Ser Tyr Glu Arg Glu
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<212> DNA

<213> Homo sapiens

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<213> Homo sapiens

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<212> DNA

<213> Homo sapiens

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tcgcagaaga	gccagcgcgc	gcagcaggtc	ctgcacctgc	aggtactgca	gcttcagcag	1020
gagaagcggc	agctccggca	ggagctcgag	agcctcatga	aggagcagga	cctgctggag	1080
accaagctca	ggtcctacga	gagggagaag	accagcttcg	gccccgcgct	ggaggagacc	1140
cagtgggagg	tgtgccagaa	gtcaggcgag	atctccctcc	tgaagcagca	gctgaaggag	1200
tcccagacgg	aggtgaacgc	caaggctagc	gagatcctgg	gtctcaaggc	acagctgaag	1260
gacacgcggg	gcaagctgga	gggcctggag	ctgaggaccc	aggacctgga	gggcgccttg	1320
cgcaccaagg	gcctggagct	ggaggtctgt	gagaatgagc	tgacgcagag	ctacgtggcc	1380
atgtaccagc	ggaaccagcg	cctggagaag	gccctgcagc	agctggcacg	tggggacagc	1440
gccggggagc	ccttggagggt	tgacctggaa	ggggctgaca	tcccctacga	ggacatcata	1500
gccactgaga	tc					1512

<210> 13
 <211> 1692
 <212> DNA
 <213> Homo sapiens

<400> 13
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 tcgcagtaca agctgcgcaa gtctctccac ctcaagaagc tcaaccggta ttccgacggg 120
 ctgctgaggt ttggcttctc ccaggactcc ggtcacggca agtccagctc caaaatgggc 180
 aagagcgaag acttcttcta catcaaggtc agccagaaag cccggggctc ccatcaccca 240
 gattacacgg cactgtccag cggggattta gggggccagg ctggggtgga ctttgacccg 300
 tccacacccc ccaagctcat gcccttctcc aatcagctag aaatgggctc cgagaagggt 360
 gcagtgaggc ccacagcctt caagcctgtg ctgccacggc caggagccat cctgcactcc 420
 tccccggaga gtgccagcca ccagctgcac cccgcccctc cagacaagcc caaggagcag 480
 gagctgaagc ctggcctgtg ctctggggcg ctgtcagact ccggccggaa ctccatgtcc 540
 agcctgcccc cacacagcac cagcagcagc taccagctgg acccgctggg cacaccctg 600
 ggaccacaaa gccgttttgg gggctccgcc cacaacatca cccagggcat cgtcctccag 660
 gacagcaaca tgatgagcct gaaggctctg tccttctccg acggaggtag caagctgggc 720
 cactcgaaca aggcagacaa gggcccctcg tgtgtccgct ccccatctc cacggacgag 780
 tgcagcatcc aggagctgga gcagaagctg ttggagaggg agggcgccct ccagaagctg 840
 cagcgcagct ttgaggagaa ggagcttgcc tccagcctgg cctacgagga gcggccgcgg 900
 cgctgcaggg acgagctgga gggcccggag cccaaaggcg gcaacaagct caagcaggcc 960
 tcgcagaaga gccagcgcgc gcagcaggct ctgcacctgc aggtactgca gcttcagcag 1020
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 tcccagacgg aggtgaacgc caaggctagc gagatcctgg gtctcaaggc acagctgaag 1260
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 gcggagctgc tgcgggagaa ggtgaacctg ctggagcggc tgcgggcca gctgcgggag 1440
 gagcggcaag gccatgacca gatgtcctcg ggcttccagc atgagcggct cgtgtggaag 1500
 gagagaaggc agaagtgat tcagtaccag aaacagctgc agcagagcta cgtggccatg 1560
 taccagcgga accagcgct ggagaaggcc ctgcagcagc tggcacgtgg ggacagcgcc 1620
 ggggagccct tggaggttga cctggaaggg gctgacatcc cctacgagga catcatagcc 1680
 actgagatct ga 1692

<210> 14
 <211> 1722
 <212> DNA
 <213> Homo sapiens

<400> 14
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 ctgctgaggt ttggcttctc ccaggactcc ggtcacggca agtccagctc caaaatgggc 180
 aagagcgaag acttcttcta catcaaggtc agccagaaag cccggggctc ccatcaccca 240
 gattacacgg cactgtccag cggggattta gggggccagg ctggggtgga ctttgacccg 300
 tccacacccc ccaagctcat gcccttctcc aatcagctag aaatgggctc cgagaagggt 360
 gcagtgaggc ccacagcctt caagcctgtg ctgccacggc caggagccat cctgcactcc 420
 tccccggaga gtgccagcca ccagctgcac cccgcccctc cagacaagcc caaggagcag 480
 gagctgaagc ctggcctgtg ctctggggcg ctgtcagact ccggccggaa ctccatgtcc 540
 agcctgcccc cacacagcac cagcagcagc taccagctgg acccgctggg cacaccctg 600
 ggaccacaaa gccgttttgg gggctccgcc cacaacatca cccagggcat cgtcctccag 660
 gacagcaaca tgatgagcct gaaggctctg tccttctccg acggaggtag caagctgggc 720

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cactcgaaca aggcagacaa gggccctcg tgtgtccgct ccccatctc cacggacgag 780
tgcagcatcc aggagctgga gcagaagctg ttggagaggg agggcgccct ccagaagctg 840
cagcgcagct ttgaggagaa ggagcttgcc tccagcctgg cctacgagga gcggccgcgg 900
cgctgcaggg acgagctgga gggcccgag cccaaaggcg gcaacaagct caagcaggcc 960
tcgcagaaga gccagcgcgc gcagcaggtc ctgcacctgc aggtactgca gcttcagcag 1020
gagaagcggc agctccggca ggagctcgag agcctcatga aggagcagga cctgctggag 1080
accaagctca ggtcctacga gagggagaag accagcttcg gccccgcgct ggaggagacc 1140
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tcccagacgg aggtgaacgc caaggctagc gagatcctgg gtctcaaggc acagctgaag 1260
gacacgctgg gcaagctgga gggcctggag ctgaggaccc aggacctgga gggcgccctg 1320
cgcaccaagg gcctggagct ggaggtctgt gagaatgagc tgcaagcga gaagaacgag 1380
gcggagctgc tgcgggagaa ggtgaacctg ctggagcagg agctgcagga gctgcgggcc 1440
caggccgccc tggcccgca catggggccg cccaccttcc ccgaggacgt ccctgccctg 1500
cagcgggagc tggagcggct cgtgtggaag gaggagaagg agaaggatgat tcagtaccag 1560
aaacagctgc agcagagcta cgtggccatg taccagcga accagcgct ggagaaggcc 1620
ctgcagcagg tggcacgtgg ggacagcgcc ggggagccct tggaggttga cctggaaggg 1680
gctgacatcc cctacgagga catcatagcc actgagatct ga 1722

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<210> 15
 <211> 76
 <212> PRT
 <213> Homo sapiens

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<400> 15
Met Gly Ser Val Ser Ser Leu Ile Ser Gly His Ser Phe His Ser Lys
 1             5             10             15

His Cys Arg Ala Ser Gln Tyr Lys Leu Arg Lys Ser Ser His Leu Lys
          20             25             30

Lys Leu Asn Arg Tyr Ser Asp Gly Leu Leu Arg Phe Gly Phe Ser Gln
          35             40             45

Asp Ser Gly His Gly Lys Ala Met Thr Arg Cys Pro Arg Ala Ser Ser
 50             55             60

Met Ser Gly Ser Cys Gly Arg Arg Arg Arg Arg Arg
 65             70             75

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<210> 16
 <211> 210
 <212> PRT
 <213> Homo sapiens

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<400> 16
Met Gly Ser Val Ser Ser Leu Ile Ser Gly His Ser Phe His Ser Lys
 1             5             10             15

His Cys Arg Ala Ser Gln Tyr Lys Leu Arg Lys Ser Ser His Leu Lys
          20             25             30

Lys Leu Asn Arg Tyr Ser Asp Gly Leu Leu Arg Phe Gly Phe Ser Gln
          35             40             45

Asp Ser Gly His Gly Lys Ser Ser Ser Lys Met Gly Lys Ser Glu Asp

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50					55					60					
Phe	Phe	Tyr	Ile	Lys	Val	Ser	Gln	Lys	Ala	Arg	Gly	Ser	His	His	Pro
65					70					75					80
Asp	Tyr	Thr	Ala	Leu	Ser	Ser	Gly	Asp	Leu	Gly	Gly	Gln	Ala	Gly	Val
				85					90					95	
Asp	Phe	Asp	Pro	Ser	Thr	Pro	Pro	Lys	Leu	Met	Pro	Phe	Ser	Asn	Gln
			100					105					110		
Leu	Glu	Met	Gly	Ser	Glu	Lys	Gly	Ala	Val	Arg	Pro	Thr	Ala	Phe	Lys
		115					120					125			
Pro	Val	Leu	Pro	Arg	Ser	Gly	Ala	Ile	Leu	His	Ser	Ser	Pro	Glu	Ser
		130				135					140				
Ala	Ser	His	Gln	Leu	His	Pro	Ala	Pro	Pro	Asp	Lys	Pro	Lys	Glu	Gln
145					150					155					160
Glu	Leu	Lys	Pro	Gly	Leu	Cys	Ser	Gly	Ala	Leu	Ser	Asp	Ser	Gly	Arg
				165					170					175	
Asn	Ser	Met	Ser	Ser	Leu	Pro	Thr	His	Ser	Ala	Gly	Glu	Pro	Leu	Glu
			180					185					190		
Val	Asp	Leu	Glu	Gly	Ala	Asp	Ile	Pro	Tyr	Glu	Asp	Ile	Ile	Ala	Thr
		195					200					205			
Glu	Ile														
	210														

<210> 17
 <211> 537
 <212> PRT
 <213> Homo sapiens

<400> 17															
Met	Gly	Ser	Val	Ser	Ser	Leu	Ile	Ser	Gly	His	Ser	Phe	His	Ser	Lys
1				5					10					15	
His	Cys	Arg	Ala	Ser	Gln	Tyr	Lys	Leu	Arg	Lys	Ser	Ser	His	Leu	Lys
			20					25					30		
Lys	Leu	Asn	Arg	Tyr	Ser	Asp	Gly	Leu	Leu	Arg	Phe	Gly	Phe	Ser	Gln
		35					40					45			
Asp	Ser	Gly	His	Gly	Lys	Ser	Ser	Ser	Lys	Met	Gly	Lys	Ser	Glu	Asp
		50				55					60				
Phe	Phe	Tyr	Ile	Lys	Val	Ser	Gln	Lys	Ala	Arg	Gly	Ser	His	His	Pro
65					70					75					80
Asp	Tyr	Thr	Ala	Leu	Ser	Ser	Gly	Asp	Leu	Gly	Gly	Gln	Ala	Gly	Val
				85					90					95	

Asp	Phe	Asp	Pro	Ser	Thr	Pro	Pro	Lys	Leu	Met	Pro	Phe	Ser	Asn	Gln		
			100					105					110				
Leu	Glu	Met	Gly	Ser	Glu	Lys	Gly	Ala	Val	Arg	Pro	Thr	Ala	Phe	Lys		
		115					120					125					
Pro	Val	Leu	Pro	Arg	Ser	Gly	Ala	Ile	Leu	His	Ser	Ser	Pro	Glu	Ser		
	130					135					140						
Ala	Ser	His	Gln	Leu	His	Pro	Ala	Pro	Pro	Asp	Lys	Pro	Lys	Glu	Gln		
145					150					155					160		
Glu	Leu	Lys	Pro	Gly	Leu	Cys	Ser	Gly	Ala	Leu	Ser	Asp	Ser	Gly	Arg		
				165					170					175			
Asn	Ser	Met	Ser	Ser	Leu	Pro	Thr	His	Ser	Thr	Ser	Ser	Ser	Tyr	Gln		
			180					185					190				
Leu	Asp	Pro	Leu	Val	Thr	Pro	Val	Gly	Pro	Thr	Ser	Arg	Phe	Gly	Gly		
	195						200					205					
Ser	Ala	His	Asn	Ile	Thr	Gln	Gly	Ile	Val	Leu	Gln	Asp	Ser	Asn	Met		
	210					215					220						
Met	Ser	Leu	Lys	Ala	Leu	Ser	Phe	Ser	Asp	Gly	Gly	Ser	Lys	Leu	Gly		
225					230					235					240		
His	Ser	Asn	Lys	Ala	Asp	Lys	Gly	Pro	Ser	Cys	Val	Arg	Ser	Pro	Ile		
			245					250						255			
Ser	Thr	Asp	Glu	Cys	Ser	Ile	Gln	Glu	Leu	Glu	Gln	Lys	Leu	Leu	Glu		
		260						265					270				
Arg	Glu	Gly	Ala	Leu	Gln	Lys	Leu	Gln	Arg	Ser	Phe	Glu	Glu	Lys	Glu		
	275						280					285					
Leu	Ala	Ser	Ser	Leu	Ala	Tyr	Glu	Glu	Arg	Pro	Arg	Arg	Cys	Arg	Asp		
	290					295					300						
Glu	Leu	Glu	Gly	Pro	Glu	Pro	Lys	Gly	Gly	Asn	Lys	Leu	Lys	Gln	Ala		
305					310					315					320		
Ser	Gln	Lys	Ser	Gln	Arg	Ala	Gln	Gln	Val	Leu	His	Leu	Gln	Val	Leu		
				325					330					335			
Gln	Leu	Gln	Gln	Glu	Lys	Arg	Gln	Leu	Arg	Gln	Glu	Leu	Glu	Ser	Leu		
			340					345					350				
Met	Lys	Glu	Gln	Asp	Leu	Leu	Glu	Thr	Lys	Leu	Arg	Ser	Tyr	Glu	Arg		
		355					360					365					
Glu	Lys	Thr	Ser	Phe	Gly	Pro	Ala	Leu	Glu	Glu	Thr	Gln	Trp	Glu	Val		
	370					375					380						
Cys	Gln	Lys	Ser	Gly	Glu	Ile	Ser	Leu	Leu	Lys	Gln	Gln	Leu	Lys	Glu		
385					390					395					400		

Ser Gln Thr Glu Val Asn Ala Lys Ala Ser Glu Ile Leu Gly Leu Lys
 405 410 415
 Ala Gln Leu Lys Asp Thr Arg Gly Lys Leu Glu Gly Leu Glu Leu Arg
 420 425 430
 Thr Gln Asp Leu Glu Gly Ala Leu Arg Thr Lys Gly Leu Glu Leu Glu
 435 440 445
 Val Cys Glu Asn Glu Leu Gln Arg Lys Lys Asn Glu Ala Glu Leu Leu
 450 455 460
 Arg Glu Lys His Glu Arg Leu Val Trp Lys Glu Glu Lys Glu Lys Val
 465 470 475 480
 Ile Gln Tyr Gln Lys Gln Leu Gln Gln Ser Tyr Val Ala Met Tyr Gln
 485 490 495
 Arg Asn Gln Arg Leu Glu Lys Ala Leu Gln Gln Leu Ala Arg Gly Asp
 500 505 510
 Ser Ala Gly Glu Pro Leu Glu Val Asp Leu Glu Gly Ala Asp Ile Pro
 515 520 525
 Tyr Glu Asp Ile Ile Ala Thr Glu Ile
 530 535

<210> 18
 <211> 504
 <212> PRT
 <213> Homo sapiens

<400> 18
 Met Gly Ser Val Ser Ser Leu Ile Ser Gly His Ser Phe His Ser Lys
 1 5 10 15
 His Cys Arg Ala Ser Gln Tyr Lys Leu Arg Lys Ser Ser His Leu Lys
 20 25 30
 Lys Leu Asn Arg Tyr Ser Asp Gly Leu Leu Arg Phe Gly Phe Ser Gln
 35 40 45
 Asp Ser Gly His Gly Lys Ser Ser Ser Lys Met Gly Lys Ser Glu Asp
 50 55 60
 Phe Phe Tyr Ile Lys Val Ser Gln Lys Ala Arg Gly Ser His His Pro
 65 70 75 80
 Asp Tyr Thr Ala Leu Ser Ser Gly Asp Leu Gly Gly Gln Ala Gly Val
 85 90 95
 Asp Phe Asp Pro Ser Thr Pro Pro Lys Leu Met Pro Phe Ser Asn Gln
 100 105 110
 Leu Glu Met Gly Ser Glu Lys Gly Ala Val Arg Pro Thr Ala Phe Lys
 115 120 125

Pro	Val	Leu	Pro	Arg	Ser	Gly	Ala	Ile	Leu	His	Ser	Ser	Pro	Glu	Ser	130	135	140
Ala	Ser	His	Gln	Leu	His	Pro	Ala	Pro	Pro	Asp	Lys	Pro	Lys	Glu	Gln	145	150	155
Glu	Leu	Lys	Pro	Gly	Leu	Cys	Ser	Gly	Ala	Leu	Ser	Asp	Ser	Gly	Arg	165	170	175
Asn	Ser	Met	Ser	Ser	Leu	Pro	Thr	His	Ser	Thr	Ser	Ser	Ser	Tyr	Gln	180	185	190
Leu	Asp	Pro	Leu	Val	Thr	Pro	Val	Gly	Pro	Thr	Ser	Arg	Phe	Gly	Gly	195	200	205
Ser	Ala	His	Asn	Ile	Thr	Gln	Gly	Ile	Val	Leu	Gln	Asp	Ser	Asn	Met	210	215	220
Met	Ser	Leu	Lys	Ala	Leu	Ser	Phe	Ser	Asp	Gly	Gly	Ser	Lys	Leu	Gly	225	230	235
His	Ser	Asn	Lys	Ala	Asp	Lys	Gly	Pro	Ser	Cys	Val	Arg	Ser	Pro	Ile	245	250	255
Ser	Thr	Asp	Glu	Cys	Ser	Ile	Gln	Glu	Leu	Glu	Gln	Lys	Leu	Leu	Glu	260	265	270
Arg	Glu	Gly	Ala	Leu	Gln	Lys	Leu	Gln	Arg	Ser	Phe	Glu	Glu	Lys	Glu	275	280	285
Leu	Ala	Ser	Ser	Leu	Ala	Tyr	Glu	Glu	Arg	Pro	Arg	Arg	Cys	Arg	Asp	290	295	300
Glu	Leu	Glu	Gly	Pro	Glu	Pro	Lys	Gly	Gly	Asn	Lys	Leu	Lys	Gln	Ala	305	310	315
Ser	Gln	Lys	Ser	Gln	Arg	Ala	Gln	Gln	Val	Leu	His	Leu	Gln	Val	Leu	325	330	335
Gln	Leu	Gln	Gln	Glu	Lys	Arg	Gln	Leu	Arg	Gln	Glu	Leu	Glu	Ser	Leu	340	345	350
Met	Lys	Glu	Gln	Asp	Leu	Leu	Glu	Thr	Lys	Leu	Arg	Ser	Tyr	Glu	Arg	355	360	365
Glu	Lys	Thr	Ser	Phe	Gly	Pro	Ala	Leu	Glu	Glu	Thr	Gln	Trp	Glu	Val	370	375	380
Cys	Gln	Lys	Ser	Gly	Glu	Ile	Ser	Leu	Leu	Lys	Gln	Gln	Leu	Lys	Glu	385	390	395
Ser	Gln	Thr	Glu	Val	Asn	Ala	Lys	Ala	Ser	Glu	Ile	Leu	Gly	Leu	Lys	405	410	415
Ala	Gln	Leu	Lys	Asp	Thr	Arg	Gly	Lys	Leu	Glu	Gly	Leu	Glu	Leu	Arg	420	425	430

Thr Gln Asp Leu Glu Gly Ala Leu Arg Thr Lys Gly Leu Glu Leu Glu
435 440 445

Val Cys Glu Asn Glu Leu Gln Gln Ser Tyr Val Ala Met Tyr Gln Arg
450 455 460

Asn Gln Arg Leu Glu Lys Ala Leu Gln Gln Leu Ala Arg Gly Asp Ser
465 470 475 480

Ala Gly Glu Pro Leu Glu Val Asp Leu Glu Gly Ala Asp Ile Pro Tyr
485 490 495

Glu Asp Ile Ile Ala Thr Glu Ile
500

<210> 19

<211> 563

<212> PRT

<213> Homo sapiens

<400> 19

Met Gly Ser Val Ser Ser Leu Ile Ser Gly His Ser Phe His Ser Lys
1 5 10 15

His Cys Arg Ala Ser Gln Tyr Lys Leu Arg Lys Ser Ser His Leu Lys
20 25 30

Lys Leu Asn Arg Tyr Ser Asp Gly Leu Leu Arg Phe Gly Phe Ser Gln
35 40 45

Asp Ser Gly His Gly Lys Ser Ser Ser Lys Met Gly Lys Ser Glu Asp
50 55 60

Phe Phe Tyr Ile Lys Val Ser Gln Lys Ala Arg Gly Ser His His Pro
65 70 75 80

Asp Tyr Thr Ala Leu Ser Ser Gly Asp Leu Gly Gly Gln Ala Gly Val
85 90 95

Asp Phe Asp Pro Ser Thr Pro Pro Lys Leu Met Pro Phe Ser Asn Gln
100 105 110

Leu Glu Met Gly Ser Glu Lys Gly Ala Val Arg Pro Thr Ala Phe Lys
115 120 125

Pro Val Leu Pro Arg Ser Gly Ala Ile Leu His Ser Ser Pro Glu Ser
130 135 140

Ala Ser His Gln Leu His Pro Ala Pro Pro Asp Lys Pro Lys Glu Gln
145 150 155 160

Glu Leu Lys Pro Gly Leu Cys Ser Gly Ala Leu Ser Asp Ser Gly Arg
165 170 175

Asn Ser Met Ser Ser Leu Pro Thr His Ser Thr Ser Ser Ser Tyr Gln

180						185						190					
Leu	Asp	Pro	Leu	Val	Thr	Pro	Val	Gly	Pro	Thr	Ser	Arg	Phe	Gly	Gly		
195						200						205					
Ser	Ala	His	Asn	Ile	Thr	Gln	Gly	Ile	Val	Leu	Gln	Asp	Ser	Asn	Met		
210						215						220					
Met	Ser	Leu	Lys	Ala	Leu	Ser	Phe	Ser	Asp	Gly	Gly	Ser	Lys	Leu	Gly		
225			230						235			240					
His	Ser	Asn	Lys	Ala	Asp	Lys	Gly	Pro	Ser	Cys	Val	Arg	Ser	Pro	Ile		
			245						250			255					
Ser	Thr	Asp	Glu	Cys	Ser	Ile	Gln	Glu	Leu	Glu	Gln	Lys	Leu	Leu	Glu		
			260						265			270					
Arg	Glu	Gly	Ala	Leu	Gln	Lys	Leu	Gln	Arg	Ser	Phe	Glu	Glu	Lys	Glu		
			275						280			285					
Leu	Ala	Ser	Ser	Leu	Ala	Tyr	Glu	Glu	Arg	Pro	Arg	Arg	Cys	Arg	Asp		
290						295						300					
Glu	Leu	Glu	Gly	Pro	Glu	Pro	Lys	Gly	Gly	Asn	Lys	Leu	Lys	Gln	Ala		
305			310						315			320					
Ser	Gln	Lys	Ser	Gln	Arg	Ala	Gln	Gln	Val	Leu	His	Leu	Gln	Val	Leu		
			325						330			335					
Gln	Leu	Gln	Gln	Glu	Lys	Arg	Gln	Leu	Arg	Gln	Glu	Leu	Glu	Ser	Leu		
			340						345			350					
Met	Lys	Glu	Gln	Asp	Leu	Leu	Glu	Thr	Lys	Leu	Arg	Ser	Tyr	Glu	Arg		
355						360						365					
Glu	Lys	Thr	Ser	Phe	Gly	Pro	Ala	Leu	Glu	Glu	Thr	Gln	Trp	Glu	Val		
370						375						380					
Cys	Gln	Lys	Ser	Gly	Glu	Ile	Ser	Leu	Leu	Lys	Gln	Gln	Leu	Lys	Glu		
385			390						395			400					
Ser	Gln	Thr	Glu	Val	Asn	Ala	Lys	Ala	Ser	Glu	Ile	Leu	Gly	Leu	Lys		
			405						410			415					
Ala	Gln	Leu	Lys	Asp	Thr	Arg	Gly	Lys	Leu	Glu	Gly	Leu	Glu	Leu	Arg		
			420			425						430					
Thr	Gln	Asp	Leu	Glu	Gly	Ala	Leu	Arg	Thr	Lys	Gly	Leu	Glu	Leu	Glu		
435						440						445					
Val	Cys	Glu	Asn	Glu	Leu	Gln	Arg	Lys	Lys	Asn	Glu	Ala	Glu	Leu	Leu		
450						455						460					
Arg	Glu	Lys	Val	Asn	Leu	Leu	Glu	Arg	Leu	Arg	Ala	Glu	Leu	Arg	Glu		
465			470						475			480					
Glu	Arg	Gln	Gly	His	Asp	Gln	Met	Ser	Ser	Gly	Phe	Gln	His	Glu	Arg		

485

490

495

Leu Val Trp Lys Glu Glu Lys Glu Lys Val Ile Gln Tyr Gln Lys Gln
500 505 510

Leu Gln Gln Ser Tyr Val Ala Met Tyr Gln Arg Asn Gln Arg Leu Glu
515 520 525

Lys Ala Leu Gln Gln Leu Ala Arg Gly Asp Ser Ala Gly Glu Pro Leu
530 535 540

Glu Val Asp Leu Glu Gly Ala Asp Ile Pro Tyr Glu Asp Ile Ile Ala
545 550 555 560

Thr Glu Ile

<210> 20

<211> 573

<212> PRT

<213> Homo sapiens

<400> 20

Met Gly Ser Val Ser Ser Leu Ile Ser Gly His Ser Phe His Ser Lys
1 5 10 15

His Cys Arg Ala Ser Gln Tyr Lys Leu Arg Lys Ser Ser His Leu Lys
20 25 30

Lys Leu Asn Arg Tyr Ser Asp Gly Leu Leu Arg Phe Gly Phe Ser Gln
35 40 45

Asp Ser Gly His Gly Lys Ser Ser Ser Lys Met Gly Lys Ser Glu Asp
50 55 60

Phe Phe Tyr Ile Lys Val Ser Gln Lys Ala Arg Gly Ser His His Pro
65 70 75 80

Asp Tyr Thr Ala Leu Ser Ser Gly Asp Leu Gly Gly Gln Ala Gly Val
85 90 95

Asp Phe Asp Pro Ser Thr Pro Pro Lys Leu Met Pro Phe Ser Asn Gln
100 105 110

Leu Glu Met Gly Ser Glu Lys Gly Ala Val Arg Pro Thr Ala Phe Lys
115 120 125

Pro Val Leu Pro Arg Ser Gly Ala Ile Leu His Ser Ser Pro Glu Ser
130 135 140

Ala Ser His Gln Leu His Pro Ala Pro Pro Asp Lys Pro Lys Glu Gln
145 150 155 160

Glu Leu Lys Pro Gly Leu Cys Ser Gly Ala Leu Ser Asp Ser Gly Arg
165 170 175

Asn	Ser	Met	Ser	Ser	Leu	Pro	Thr	His	Ser	Thr	Ser	Ser	Ser	Tyr	Gln	180	185	190	
Leu	Asp	Pro	Leu	Val	Thr	Pro	Val	Gly	Pro	Thr	Ser	Arg	Phe	Gly	Gly	195	200	205	
Ser	Ala	His	Asn	Ile	Thr	Gln	Gly	Ile	Val	Leu	Gln	Asp	Ser	Asn	Met	210	215	220	
Met	Ser	Leu	Lys	Ala	Leu	Ser	Phe	Ser	Asp	Gly	Gly	Ser	Lys	Leu	Gly	225	230	235	240
His	Ser	Asn	Lys	Ala	Asp	Lys	Gly	Pro	Ser	Cys	Val	Arg	Ser	Pro	Ile	245	250	255	
Ser	Thr	Asp	Glu	Cys	Ser	Ile	Gln	Glu	Leu	Glu	Gln	Lys	Leu	Leu	Glu	260	265	270	
Arg	Glu	Gly	Ala	Leu	Gln	Lys	Leu	Gln	Arg	Ser	Phe	Glu	Glu	Lys	Glu	275	280	285	
Leu	Ala	Ser	Ser	Leu	Ala	Tyr	Glu	Glu	Arg	Pro	Arg	Arg	Cys	Arg	Asp	290	295	300	
Glu	Leu	Glu	Gly	Pro	Glu	Pro	Lys	Gly	Gly	Asn	Lys	Leu	Lys	Gln	Ala	305	310	315	320
Ser	Gln	Lys	Ser	Gln	Arg	Ala	Gln	Gln	Val	Leu	His	Leu	Gln	Val	Leu	325	330	335	
Gln	Leu	Gln	Gln	Glu	Lys	Arg	Gln	Leu	Arg	Gln	Glu	Leu	Glu	Ser	Leu	340	345	350	
Met	Lys	Glu	Gln	Asp	Leu	Leu	Glu	Thr	Lys	Leu	Arg	Ser	Tyr	Glu	Arg	355	360	365	
Glu	Lys	Thr	Ser	Phe	Gly	Pro	Ala	Leu	Glu	Glu	Thr	Gln	Trp	Glu	Val	370	375	380	
Cys	Gln	Lys	Ser	Gly	Glu	Ile	Ser	Leu	Leu	Lys	Gln	Gln	Leu	Lys	Glu	385	390	395	400
Ser	Gln	Thr	Glu	Val	Asn	Ala	Lys	Ala	Ser	Glu	Ile	Leu	Gly	Leu	Lys	405	410	415	
Ala	Gln	Leu	Lys	Asp	Thr	Arg	Gly	Lys	Leu	Glu	Gly	Leu	Glu	Leu	Arg	420	425	430	
Thr	Gln	Asp	Leu	Glu	Gly	Ala	Leu	Arg	Thr	Lys	Gly	Leu	Glu	Leu	Glu	435	440	445	
Val	Cys	Glu	Asn	Glu	Leu	Gln	Arg	Lys	Lys	Asn	Glu	Ala	Glu	Leu	Leu	450	455	460	
Arg	Glu	Lys	Val	Asn	Leu	Leu	Glu	Gln	Glu	Leu	Gln	Glu	Leu	Arg	Ala	465	470	475	480

Gln Ala Ala Leu Ala Arg Asp Met Gly Pro Pro Thr Phe Pro Glu Asp
485 490 495

Val Pro Ala Leu Gln Arg Glu Leu Glu Arg Leu Val Trp Lys Glu Glu
500 505 510

Lys Glu Lys Val Ile Gln Tyr Gln Lys Gln Leu Gln Gln Ser Tyr Val
515 520 525

Ala Met Tyr Gln Arg Asn Gln Arg Leu Glu Lys Ala Leu Gln Gln Leu
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Ala Arg Gly Asp Ser Ala Gly Glu Pro Leu Glu Val Asp Leu Glu Gly
545 550 555 560

Ala Asp Ile Pro Tyr Glu Asp Ile Ile Ala Thr Glu Ile
565 570

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<211> 591
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<220>
<223> Description of Artificial Sequence: F37 Probe

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gcttttgaca gcttcatttt atttttgacg tcactttttg gccatgtaaa ctatttgtgg 540
caattttatg tttttattta tgaataaaga atgccatttc tcacgccctc t 591

<210> 22
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: FEZ1 alterable
region amplificatin primer G12

<400> 22
gctgccacag cctttccaag acc

23

<210> 23
<211> 23
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: FEZ1 alterable
region amplification primer G13

<400> 23

taccggttga gcttcttgag gtg

23

<210> 24

<211> 23

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: FEZ1 alterable
region amplification primer G14.2

<400> 24

acagcttcca cagcaagcac tgc

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<210> 25

<211> 21

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: FEZ1 alterable
region amplification primer G15

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attggagaag ggcatgagct t

21

<210> 26

<211> 22

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: FEZ1 alterable
region amplification primer G16

<400> 26

tggactttga cccgtccaca cc

22

<210> 27

<211> 23

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: FEZ1 alterable
region amplification primer IntABR

<400> 27
gtttccaacc cacttaccct tgc 23

<210> 28
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
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region amplification primer IntABF

<400> 28
gcaggggagg catgagtcac c 21

<210> 29
<211> 22
<212> DNA
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region amplification primer G17

<400> 29
ggcttcagct cctgctcctt gg 22

<210> 30
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region amplification primer G20

<400> 30
acaacatcac ccagggcac gtc 23

<210> 31
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<212> DNA
<213> Artificial Sequence

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region amplification primer G21

<400> 31
cctccagctc gtcctgcag c 21

<210> 32

<211> 23
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 region amplification primer G32

 <400> 32
 actgcagctt cagcaggaga agc 23

 <210> 33
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 <212> DNA
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 <223> Description of Artificial Sequence: FEZ1 alterable
 region amplification primer IntBCR

 <400> 33
 ctgaccaccc aaacccatga gc 22

 <210> 34
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 <212> DNA
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 <223> Description of Artificial Sequence: FEZ1 alterable
 region amplification primer IntBCF

 <400> 34
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 <210> 35
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 <212> DNA
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 <223> Description of Artificial Sequence: FEZ1 alterable
 region amplification primer Mut6

 <400> 35
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 <210> 36
 <211> 23
 <212> DNA
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<223> Description of Artificial Sequence: FEZ1 alterable
region amplification primer G1

<400> 36

tgaacgccaa ggctagcgag atc

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<210> 37

<211> 22

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: FEZ1 alterable
region amplification primer G2

<400> 37

gctcctgcag ctctgctcc ag

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<210> 38

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: FEZ1 alterable
region amplification primer G75

<400> 38

cccaccttcc ccgaggacgt c

21

<210> 39

<211> 23

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: FEZ1 alterable
region amplification primer G82

<400> 39

agcccgagga catctgggtca tgg

23

<210> 40

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: FEZ1 alterable
region amplification primer G5

<400> 40

cctgccctgc agcgggagct ggag

24

<210> 41
<211> 23
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<220>
<223> Description of Artificial Sequence: FEZ1 alterable
region amplification primer G6

<400> 41
agctgctgca gggccttctc cag 23

<210> 42
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<223> Description of Artificial Sequence: FEZ1 alterable
region amplification primer G7

<400> 42
cagtaccaga aacagctgca gcagagc 27

<210> 43
<211> 22
<212> DNA
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<220>
<223> Description of Artificial Sequence: FEZ1 alterable
region amplification primer G8

<400> 43
ccctgcctcc cagtgccagg tc 22

<210> 44
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: First strand
of partially-double stranded adapter-linker

<400> 44
gatctcgacg aattcgtgag acct 24

<210> 45
<211> 20
<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Second strand
of partially-double stranded adapter-linker

<400> 45

tggtctcacg aattcgtcga

20

<210> 46

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Donor site
sequence of truncated FEZ1 truncation region

<400> 46

tcccaggact ccggtcacgg caa

23

<210> 47

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Acceptor site
sequence of truncated FEZ1 truncation region

<400> 47

gagcggcaag gccatgacca g

21

<210> 48

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Donor site
sequence of truncated FEZ1 truncation region

<400> 48

agcctgcca cacacagcac cag

23

<210> 49

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Acceptor site
sequence of truncated FEZ1 truncation region

<400> 49
cagcgccggg gagcccttgg a 21

<210> 50
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Donor site
sequence of truncated FEZ1 truncation region

<400> 50
gtgagaatga gctgcagcgc aag 23

<210> 51
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Acceptor site
sequence of truncated FEZ1 truncation region

<400> 51
cagcagagct acgtggccat gt 22

<210> 52
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Donor site
sequence of truncated FEZ1 truncation region

<400> 52
agctgctgcg ggagaagggtg aac 23

<210> 53
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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Acceptor site
sequence of truncated FEZ1 truncation region

<400> 53
cagcatgagc ggctcgtgtg ga 22

<210> 54
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Donor site
sequence of truncated FEZ1 truncation region

<400> 54
aggtgaacct gctggagcag gag 23

<210> 55
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Acceptor site
sequence of truncated FEZ1 truncation region

<400> 55
gagcggctgc gggccgagct gc 22

<210> 56
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Donor site
sequence of truncated FEZ1 truncation region

<400> 56
ctgcagcggg agctggagcg gctg 24

<210> 57
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Acceptor site
sequence of truncated FEZ1 truncation region

<400> 57
gagcggctcg tgtggaagga g 21

<210> 58
<211> 27
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer for
amplifying FEZ1 cDNA

<400> 58

cagatgggca gcgtcagtag cctcatc

27

<210> 59

<211> 24

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer for
amplifying FEZ1 cDNA

<400> 59

tcagatctca gtggctatga tgtc

24

<210> 60

<211> 8073

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Nucleotide
sequence of vector pQBI-AdCMV5-IRES-GFP

<400> 60

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agtgcggtt	ttggtgtgcg	ccggtgtaca	caggaagtga	caattttcgc	gcggttttag	240
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